

## BLAST

### Basic Local Alignment Search Tool

- Your search parameters were adjusted to search for a short input sequence.

[Edit](#) [and Resubmit](#) [Save Search Strategies](#) [Formatting options](#) [Download](#)

#### Protein Sequence (15 letters)

residues 66-80 of SEQ ID NO: 12

Results for:

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

#### Query ID

|cl|41354

|cl|41354

#### Description

None

#### Molecule type

amino acid

#### Query Length

15

#### Database Name

nr

#### Description

All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects

#### Program

BLASTP 2.2.22+ [Citation](#)

#### Reference

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", *Nucleic Acids Res.* 25:3389-3402.

Other reports: [Search Summary](#) [\[Taxonomy reports\]](#) [\[Multiple alignment\]](#) [NEW](#)

### Search Parameters

|               |        |
|---------------|--------|
| Program       | blastp |
| Word size     | 2      |
| Expect value  | 200000 |
| Hitlist size  | 100    |
| Gapcosts      | 9,1    |
| Matrix        | PAM30  |
| Threshold     | 11     |
| Filter string | F      |
| Genetic Code  | 1      |
| Window Size   | 40     |

### Database

|                     |                     |
|---------------------|---------------------|
| Posted date         | Jan 3, 2010 5:44 PM |
| Number of letters   | 3,505,793,397       |
| Number of sequences | 10,274,250          |
| Entrez query        | none                |

### Karlin-Altschul statistics

|        |          |        |
|--------|----------|--------|
| Params | Unapped  | Gapped |
| Lambda | 0.358076 | 0.294  |
| K      | 0.289736 | 0.11   |
| H      | 1.81294  | 0.61   |

### Results Statistics

|                              |             |
|------------------------------|-------------|
| Length adjustment            | 5           |
| Effective length of query    | 10          |
| Effective length of database | 3454422147  |
| Effective search space       | 34544221470 |
| Effective search space used  | 34544221470 |

[Graphic Summary](#)

[Show Conserved Domains](#)

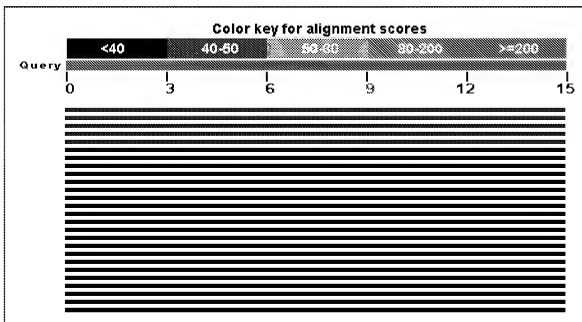
No putative conserved domains have been detected

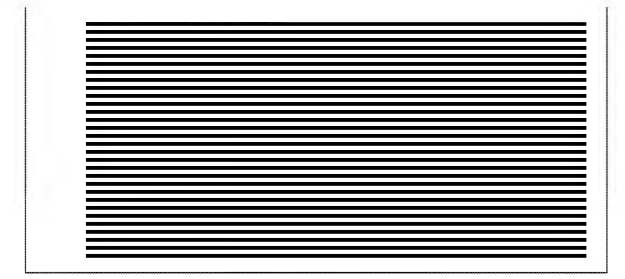


### Distribution of 100 Blast Hits on the Query Sequence



An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.





## Descriptions

| E             | Sequences producing significant alignments:       | Score  |       |
|---------------|---|--------|-------|
|               |   | (Bits) | Value |
| gb ABU97123.1 | S protein [Hepatitis B virus]                     | 43.5   | 0.003 |
| gb ABU17005.1 | surface antigen [Hepatitis B virus]               | 43.5   | 0.003 |
| gb BAG12008.1 | S protein [Hepatitis B virus]                     | 42.5   | 0.003 |
| gb AAW65562.1 | HBsAg [Hepatitis B virus]                         | 43.5   | 0.003 |
| gb AAP13661.1 | surface antigen [Hepatitis B virus]               | 42.2   | 0.007 |
| gb ACX36965.1 | middle S protein [Hepatitis B virus] >gb ACX36... | 39.7   | 0.040 |
| gb ACX36957.1 | middle S protein [Hepatitis B virus]              | 39.7   | 0.040 |
| gb BAG64746.1 | hepatitis B surface antigen [Hepatitis B virus]   | 39.7   | 0.040 |
| gb ACQ82752.1 | S protein [Hepatitis B virus]                     | 38.8   | 0.072 |
| gb ACQ82751.1 | middle S protein [Hepatitis B virus]              | 38.8   | 0.072 |
| gb ACQ82750.1 | large S protein [Hepatitis B virus]               | 38.8   | 0.072 |
| gb BAH84154.1 | hepatitis B surface antigen [Hepatitis B virus]   | 38.8   | 0.072 |
| gb BAH84102.1 | hepatitis B surface antigen [Hepatitis B virus]   | 38.8   | 0.072 |
| gb BAH83930.1 | hepatitis B surface antigen [Hepatitis B virus]   | 38.8   | 0.072 |
| gb ACJ66248.1 | middle S protein [Hepatitis B virus]              | 38.8   | 0.072 |
| gb ACJ66247.1 | large S protein [Hepatitis B virus]               | 38.8   | 0.072 |
| gb ACJ66242.1 | S protein [Hepatitis B virus]                     | 38.8   | 0.072 |
| gb ACJ66241.1 | middle S protein [Hepatitis B virus]              | 38.8   | 0.072 |
| gb ACJ66240.1 | large S protein [Hepatitis B virus]               | 38.8   | 0.072 |
| gb ACJ66233.1 | large S protein [Hepatitis B virus]               | 38.8   | 0.072 |
| gb ACJ66236.1 | S protein [Hepatitis B virus]                     | 38.8   | 0.072 |
| gb ACJ66237.1 | middle S protein [Hepatitis B virus]              | 38.8   | 0.072 |
| gb ACJ66236.1 | large S protein [Hepatitis B virus]               | 38.8   | 0.072 |
| gb ACJ66213.1 | middle S protein [Hepatitis B virus]              | 38.8   | 0.072 |
| gb ACJ66212.1 | large S protein [Hepatitis B virus]               | 38.8   | 0.072 |
| gb ACJ66207.1 | S protein [Hepatitis B virus]                     | 38.8   | 0.072 |
| gb ACJ66206.1 | middle S protein [Hepatitis B virus]              | 38.8   | 0.072 |
| gb ACJ66205.1 | large S protein [Hepatitis B virus]               | 38.8   | 0.072 |
| gb ACJ66164.1 | middle S protein [Hepatitis B virus]              | 38.8   | 0.072 |
| gb ACJ66163.1 | large S protein [Hepatitis B virus]               | 38.8   | 0.072 |
| gb ACJ66136.1 | middle S protein [Hepatitis B virus] >gb ACJ66... | 38.8   | 0.072 |
| gb ACJ66135.1 | large S protein [Hepatitis B virus] >gb ACJ661... | 38.8   | 0.072 |
| gb ACJ66130.1 | S protein [Hepatitis B virus]                     | 38.8   | 0.072 |
| gb ACJ66129.1 | middle S protein [Hepatitis B virus]              | 38.8   | 0.072 |
| gb ACJ66128.1 | large S protein [Hepatitis B virus]               | 38.8   | 0.072 |
| gb ACJ66122.1 | large S protein [Hepatitis B virus]               | 38.8   | 0.072 |
| gb ACJ66096.1 | S protein [Hepatitis B virus]                     | 38.8   | 0.072 |
| gb ACJ66095.1 | large S protein [Hepatitis B virus]               | 38.8   | 0.072 |
| gb ACJ66091.1 | large S protein [Hepatitis B virus] >gb ACJ660... | 38.8   | 0.072 |
| gb ACJ66006.1 | S protein [Hepatitis B virus]                     | 38.8   | 0.072 |
| gb ACJ66005.1 | middle S protein [Hepatitis B virus]              | 38.8   | 0.072 |
| gb ACJ66004.1 | large S protein [Hepatitis B virus]               | 38.8   | 0.072 |
| gb ACJ66007.1 | middle S protein [Hepatitis B virus]              | 38.8   | 0.072 |
| gb ACJ66006.1 | large S protein [Hepatitis B virus]               | 38.8   | 0.072 |
| gb ACJ66059.1 | S protein [Hepatitis B virus]                     | 38.8   | 0.072 |
| gb ACJ66058.1 | middle S protein [Hepatitis B virus]              | 38.8   | 0.072 |
| gb ACJ66057.1 | large S protein [Hepatitis B virus]               | 38.8   | 0.072 |
| gb ACR66199.1 | large S protein [Hepatitis B virus]               | 38.8   | 0.072 |
| gb ACR66193.1 | large S protein [Hepatitis B virus]               | 38.8   | 0.072 |
| gb ACR66192.1 | large S protein [Hepatitis B virus]               | 38.8   | 0.072 |
| gb ACR66180.1 | large S protein [Hepatitis B virus]               | 38.8   | 0.072 |
| gb ACR66170.1 | large S protein [Hepatitis B virus]               | 38.8   | 0.072 |
| gb ACR66160.1 | large S protein [Hepatitis B virus]               | 38.8   | 0.072 |
| gb ACR66122.1 | large S protein [Hepatitis B virus]               | 38.8   | 0.072 |
| gb ACR66138.1 | large S protein [Hepatitis B virus]               | 38.8   | 0.072 |
| gb ACR66129.1 | large S protein [Hepatitis B virus]               | 38.8   | 0.072 |
| gb ACR66123.1 | large S protein [Hepatitis B virus]               | 38.8   | 0.072 |

Alignments Select All Get selected sequences Distance tree of results Multiple alignment NEW

Query 1 PLIPGSTRTSTGQCK 15  
PLIPGST TSTGQCK

Sbjct 1 PLIPGSTRITSGQCK 15

>dbj|BAG12008.1| S protein [Hepatitis B virus]  
Length=254

Score = 43.5 bits (95), Expect = 0.003  
Identities = 14/15 (93%), Positives = 14/15 (93%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRITSGQCK 15  
PLIPGST TSTGQCK  
Sbjct 136 PLIPGSTRITSGQCK 150

>gb|AAW65562.1| HBsAg [Hepatitis B virus]  
Length=226

Score = 43.5 bits (95), Expect = 0.003  
Identities = 14/15 (93%), Positives = 14/15 (93%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRITSGQCK 15  
PLIPGST TSTGQCK  
Sbjct 108 PLIPGSTRITSGQCK 122

>gb|AAD13661.1| surface antigen [Hepatitis B virus]  
Length=226

Score = 42.2 bits (92), Expect = 0.007  
Identities = 13/15 (86%), Positives = 14/15 (93%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRITSGQCK 15  
PLIPGSTRITSG CK  
Sbjct 108 PLIPGSTRITSGPCK 122

>gb|ACX36965.1| middle S protein [Hepatitis B virus]  
>gb|ACX36975.1| middle S protein [Hepatitis B virus]  
Length=243

Score = 39.7 bits (86), Expect = 0.040  
Identities = 13/15 (86%), Positives = 14/15 (93%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRITSGQCK 15  
PLPGST TSTGQCK  
Sbjct 125 PLLPGSTRITSGQCK 139

>gb|ACX36957.1| middle S protein [Hepatitis B virus]  
Length=243

Score = 39.7 bits (86), Expect = 0.040  
Identities = 13/15 (86%), Positives = 14/15 (93%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRITSGQCK 15  
PLPGST TSTGQCK  
Sbjct 125 PLLPGSTRITSGQCK 139

>dbj|BAG06746.1| hepatitis B surface antigen [Hepatitis B virus]  
Length=132

Score = 39.7 bits (86), Expect = 0.040  
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRITSGQCK 15  
PLIPGST TSTG CK  
Sbjct 69 PLIPGSTRITSGXCK 83

>gb|ACQ82752.1| S protein [Hepatitis B virus]  
Length=226

Score = 38.8 bits (84), Expect = 0.072  
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRITSGQCK 15  
PLIPGST TSTG CK  
Sbjct 108 PLIPGSTRITSGPCK 122

>gb|ACQ82751.1| middle S protein [Hepatitis B virus]  
Length=281

Score = 38.8 bits (84), Expect = 0.072  
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRITSGQCK 15  
PLIPGST TSTG CK  
Sbjct 163 PLIPGSTTTTSGPCK 177

>gb|ACQ82750.1| large S protein [Hepatitis B virus]  
Length=400

Score = 38.8 bits (84), Expect = 0.072  
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRITSGQCK 15  
PLIPGST TSTG CK  
Sbjct 282 PLIPGSTTTTSGPCK 296

>dbj|BAH84154.1| hepatitis B surface antigen [Hepatitis B virus]  
Length=132

Score = 38.8 bits (84), Expect = 0.072  
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRITSGQCK 15  
PLIPGST TSTG CK  
Sbjct 69 PLIPGSTTTTSGPCK 83

>dbj|BAH84102.1| hepatitis B surface antigen [Hepatitis B virus]  
Length=132

Score = 38.8 bits (84), Expect = 0.072  
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRITSGQCK 15  
PLIPGST TSTG CK  
Sbjct 69 PLIPGSTTTTSGPCK 83

>dbj|BAH83930.1| hepatitis B surface antigen [Hepatitis B virus]  
Length=132

Score = 38.8 bits (84), Expect = 0.072  
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRITSGQCK 15  
PLIPGST TSTG CK  
Sbjct 69 PLIPGSTTTTSGPCK 83

>gb|ACJ66248.1| middle S protein [Hepatitis B virus]  
Length=281

Score = 38.8 bits (84), Expect = 0.072  
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRITSGQCK 15  
PLIPGST TSTG CK  
Sbjct 163 PLIPGSTTTTSGPCK 177

>gb|ACJ66247.1| large S protein [Hepatitis B virus]  
Length=400

Score = 38.8 bits (84), Expect = 0.072  
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRITSGQCK 15  
PLIPGST TSTG CK  
Sbjct 282 PLIPGSTTTTSGPCK 296

>gb|ACJ66242.1| S protein [Hepatitis B virus]  
Length=226

Score = 38.8 bits (84), Expect = 0.072  
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRISTGQCK 15  
          PLIPGST ISTG CK  
Sbjct 108 PLIPGSTTTSTGPCK 122

>gb|ACJ66241.1| middle S protein [Hepatitis B virus]  
Length=281

Score = 38.8 bits (84), Expect = 0.072  
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRISTGQCK 15  
          PLIPGST ISTG CK  
Sbjct 163 PLIPGSTTTSTGPCK 177

>gb|ACJ66240.1| large S protein [Hepatitis B virus]  
Length=400

Score = 38.8 bits (84), Expect = 0.072  
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRISTGQCK 15  
          PLIPGST ISTG CK  
Sbjct 282 PLIPGSTTTSTGPCK 296

>gb|ACJ66233.1| large S protein [Hepatitis B virus]  
Length=400

Score = 38.8 bits (84), Expect = 0.072  
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRISTGQCK 15  
          PLIPGST ISTG CK  
Sbjct 282 PLIPGSTTTSTGPCK 296

>gb|ACJ66228.1| S protein [Hepatitis B virus]  
Length=226

Score = 38.8 bits (84), Expect = 0.072  
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRISTGQCK 15  
          PLIPGST ISTG CK  
Sbjct 108 PLIPGSTTTSTGPCK 122

>gb|ACJ66227.1| middle S protein [Hepatitis B virus]  
Length=281

Score = 38.8 bits (84), Expect = 0.072  
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRISTGQCK 15  
          PLIPGST ISTG CK  
Sbjct 163 PLIPGSTTTSTGPCK 177

>gb|ACJ66226.1| large S protein [Hepatitis B virus]  
Length=400

Score = 38.8 bits (84), Expect = 0.072  
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRISTGQCK 15  
          PLIPGST ISTG CK  
Sbjct 282 PLIPGSTTTSTGPCK 296

>gb|ACJ66213.1| middle S protein [Hepatitis B virus]  
Length=281

Score = 38.8 bits (84), Expect = 0.072  
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)



Query 1 PLIPGSTRISTGQCK 15  
 Sbjct 163 PLIPGSTTSTGPK 177

>gb|ACJ66212.1| large S protein [Hepatitis B virus]  
 Length=400

Score = 38.8 bits (84), Expect = 0.072  
 Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRISTGQCK 15  
 Sbjct 282 PLIPGSTTSTGPK 296

>gb|ACJ66207.1| S protein [Hepatitis B virus]  
 Length=226

Score = 38.8 bits (84), Expect = 0.072  
 Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRISTGQCK 15  
 Sbjct 108 PLIPGSTTSTGPK 122

>gb|ACJ66206.1| middle S protein [Hepatitis B virus]  
 Length=279

Score = 38.8 bits (84), Expect = 0.072  
 Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRISTGQCK 15  
 Sbjct 161 PLIPGSTTSTGPK 175

>gb|ACJ66205.1| large S protein [Hepatitis B virus]  
 Length=398

Score = 38.8 bits (84), Expect = 0.072  
 Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRISTGQCK 15  
 Sbjct 280 PLIPGSTTSTGPK 294

>gb|ACJ66164.1| middle S protein [Hepatitis B virus]  
 Length=281

Score = 38.8 bits (84), Expect = 0.072  
 Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRISTGQCK 15  
 Sbjct 163 PLIPGSTTSTGPK 177

>gb|ACJ66163.1| large S protein [Hepatitis B virus]  
 Length=400

Score = 38.8 bits (84), Expect = 0.072  
 Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRISTGQCK 15  
 Sbjct 282 PLIPGSTTSTGPK 296

>gb|ACJ66136.1| middle S protein [Hepatitis B virus]  
 gb|ACJ66178.1| middle S protein [Hepatitis B virus]  
 gb|ACJ66192.1| middle S protein [Hepatitis B virus]  
 gb|ACJ66198.1| middle S protein [Hepatitis B virus]  
 Length=281

Score = 38.8 bits (84), Expect = 0.072  
 Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRISTGQCK 15  
 PLIPGST ISTG CK  
 Sbjct 163 PLIPGSTITTSTGPCK 177

>gb|ACJ66135.1| large S protein [Hepatitis B virus]  
 gb|ACJ66177.1| large S protein [Hepatitis B virus]  
 gb|ACJ66191.1| large S protein [Hepatitis B virus]  
 gb|ACJ66203.1| large S protein [Hepatitis B virus]  
 Length=400

Score = 38.8 bits (84), Expect = 0.072  
 Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRISTGQCK 15  
 PLIPGST ISTG CK  
 Sbjct 282 PLIPGSTITTSTGPCK 296

>gb|ACJ66130.1| S protein [Hepatitis B virus]  
 Length=226

Score = 38.8 bits (84), Expect = 0.072  
 Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRISTGQCK 15  
 PLIPGST ISTG CK  
 Sbjct 108 PLIPGSTITTSTGPCK 122

>gb|ACJ66129.1| middle S protein [Hepatitis B virus]  
 Length=281

Score = 38.8 bits (84), Expect = 0.072  
 Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRISTGQCK 15  
 PLIPGST ISTG CK  
 Sbjct 163 PLIPGSTITTSTGPCK 177

>gb|ACJ66128.1| large S protein [Hepatitis B virus]  
 Length=400

Score = 38.8 bits (84), Expect = 0.072  
 Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRISTGQCK 15  
 PLIPGST ISTG CK  
 Sbjct 282 PLIPGSTITTSTGPCK 296

>gb|ACJ66122.1| large S protein [Hepatitis B virus]  
 Length=400

Score = 38.8 bits (84), Expect = 0.072  
 Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRISTGQCK 15  
 PLIPGST ISTG CK  
 Sbjct 282 PLIPGSTITTSTGPCK 296

>gb|ACJ66096.1| S protein [Hepatitis B virus]  
 Length=226

Score = 38.8 bits (84), Expect = 0.072  
 Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRISTGQCK 15  
 PLIPGST ISTG CK  
 Sbjct 108 PLIPGSTITTSTGPCK 122

>gb|ACJ66095.1| large S protein [Hepatitis B virus]  
 Length=400

Score = 38.8 bits (84), Expect = 0.072  
 Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRISTGQCK 15  
 PLIPGST TSTG CK  
 Sbjct 282 PLIPGTTTSTGPK 296

>gb|ACJ66081.1| large S protein [Hepatitis B virus]  
 gb|ACJ66088.1| large S protein [Hepatitis B virus]  
 gb|ACJ66142.1| large S protein [Hepatitis B virus]  
 gb|ACJ66156.1| large S protein [Hepatitis B virus]  
 Length=400

Score = 38.8 bits (84), Expect = 0.072  
 Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRISTGQCK 15  
 PLIPGST TSTG CK  
 Sbjct 282 PLIPGTTTSTGPK 296

>gb|ACJ66006.1| S protein [Hepatitis B virus]  
 Length=226

Score = 38.8 bits (84), Expect = 0.072  
 Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRISTGQCK 15  
 PLIPGST TSTG CK  
 Sbjct 108 PLIPGTTTSTGPK 122

>gb|ACJ66005.1| middle S protein [Hepatitis B virus]  
 Length=281

Score = 38.8 bits (84), Expect = 0.072  
 Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRISTGQCK 15  
 PLIPGST TSTG CK  
 Sbjct 163 PLIPGTTTSTGPK 177

>gb|ACJ66004.1| large S protein [Hepatitis B virus]  
 Length=400

Score = 38.8 bits (84), Expect = 0.072  
 Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRISTGQCK 15  
 PLIPGST TSTG CK  
 Sbjct 282 PLIPGTTTSTGPK 296

>gb|ACJ65907.1| middle S protein [Hepatitis B virus]  
 Length=281

Score = 38.8 bits (84), Expect = 0.072  
 Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRISTGQCK 15  
 PLIPGST TSTG CK  
 Sbjct 163 PLIPGTTTSTGPK 177

>gb|ACJ65906.1| large S protein [Hepatitis B virus]  
 Length=400

Score = 38.8 bits (84), Expect = 0.072  
 Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRISTGQCK 15  
 PLIPGST TSTG CK  
 Sbjct 282 PLIPGTTTSTGPK 296

>gb|ACJ65859.1| S protein [Hepatitis B virus]  
 Length=226

Score = 38.8 bits (84), Expect = 0.072  
 Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRITSGQCK 15  
          PLIPGST ITSG CK  
Sbjct 108 PLIPGSTTTTSGPCK 122

>gb|ACJ65858.1| middle S protein [Hepatitis B virus]  
Length=281

Score = 38.8 bits (84), Expect = 0.072  
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRITSGQCK 15  
          PLIPGST ITSG CK  
Sbjct 163 PLIPGSTTTTSGPCK 177

>gb|ACJ65857.1| large S protein [Hepatitis B virus]  
Length=400

Score = 38.8 bits (84), Expect = 0.072  
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRITSGQCK 15  
          PLIPGST ITSG CK  
Sbjct 282 PLIPGSTTTTSGPCK 296

>gb|ACR66198.1| large S protein [Hepatitis B virus]  
Length=215

Score = 38.8 bits (84), Expect = 0.072  
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRITSGQCK 15  
          PLIPGST ITSG CK  
Sbjct 120 PLIPGSTTTTSGPCK 134

>gb|ACR66183.1| large S protein [Hepatitis B virus]  
Length=215

Score = 38.8 bits (84), Expect = 0.072  
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRITSGQCK 15  
          PLIPGST ITSG CK  
Sbjct 120 PLIPGSTTTTSGPCK 134

>gb|ACR66182.1| large S protein [Hepatitis B virus]  
Length=215

Score = 38.8 bits (84), Expect = 0.072  
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRITSGQCK 15  
          PLIPGST ITSG CK  
Sbjct 120 PLIPGSTTTTSGPCK 134

>gb|ACR66180.1| large S protein [Hepatitis B virus]  
Length=215

Score = 38.8 bits (84), Expect = 0.072  
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRITSGQCK 15  
          PLIPGST ITSG CK  
Sbjct 120 PLIPGSTTTTSGPCK 134

>gb|ACR66170.1| large S protein [Hepatitis B virus]  
Length=215

Score = 38.8 bits (84), Expect = 0.072  
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRITSGQCK 15  
          PLIPGST ITSG CK

Sbjct 120 PLIPGSTTTSTGPCK 134

>gb|ACR66160.1| large S protein [Hepatitis B virus]  
Length=215

Score = 38.8 bits (84), Expect = 0.072  
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRITSGQCK 15  
PLIPGST ITSG CK  
Sbjct 120 PLIPGSTTTSTGPCK 134

>gb|ACR66152.1| large S protein [Hepatitis B virus]  
Length=215

Score = 38.8 bits (84), Expect = 0.072  
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRITSGQCK 15  
PLIPGST ITSG CK  
Sbjct 120 PLIPGSTTTSTGPCK 134

>gb|ACR66138.1| large S protein [Hepatitis B virus]  
Length=215

Score = 38.8 bits (84), Expect = 0.072  
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRITSGQCK 15  
PLIPGST ITSG CK  
Sbjct 120 PLIPGSTTTSTGPCK 134

>gb|ACR66129.1| large S protein [Hepatitis B virus]  
Length=215

Score = 38.8 bits (84), Expect = 0.072  
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRITSGQCK 15  
PLIPGST ITSG CK  
Sbjct 120 PLIPGSTTTSTGPCK 134

>gb|ACR66123.1| large S protein [Hepatitis B virus]  
Length=215

Score = 38.8 bits (84), Expect = 0.072  
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRITSGQCK 15  
PLIPGST ITSG CK  
Sbjct 120 PLIPGSTTTSTGPCK 134

>gb|ACR66097.1| large S protein [Hepatitis B virus]  
>gb|ACR66110.1| large S protein [Hepatitis B virus]  
Length=215

Score = 38.8 bits (84), Expect = 0.072  
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRITSGQCK 15  
PLIPGST ITSG CK  
Sbjct 120 PLIPGSTTTSTGPCK 134

>gb|ACR66094.1| large S protein [Hepatitis B virus]  
Length=215

Score = 38.8 bits (84), Expect = 0.072  
Identities = 13/15 (86%), Positives = 13/15 (86%), Gaps = 0/15 (0%)

Query 1 PLIPGSTRITSGQCK 15  
PLIPGST ITSG CK  
Sbjct 120 PLIPGSTTTSTGPCK 134